

1     IN THE CLAIMS

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3             Please amend the claims as follows:

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5     --1. **(Currently Amended)**   A method for analyzing a ~~complex~~ biological sample using a Fourier  
6     Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 7             a.     ionizing a drug-dosed biological sample to produce sample (molecular) ions;
- 8             b.     introducing said ions into an analysis region of said FTMS;
- 9             c.     analyzing said ions to determine the molecular weight and abundance of said ions;
- 10            d.     utilizing said molecular weight to determine the empirical formula of each species of said
- 11            sample; and
- 12            e.     identifying each said species by comparing said empirical formula to a database of
- 13            formulas for known molecules.

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15     2. **(Original)**   A method according to claim 1, wherein said determining of the molecular weight is  
16     performed with an accuracy sufficient to identify empirical formula of said ions.

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18     3. **(Currently Amended)**   A method according to claim 1, wherein said database of known  
19     molecules is updated with said determined ~~molecular structures~~ empirical formulas.

1     **4. (Currently Amended)**     A method for analyzing a ~~complex~~ biological sample using a Fourier  
2     Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 3             a.     ionizing a drug-dosed biological sample to produce sample (molecular) ions;
- 4             b.     introducing said ions into an analysis region of said FTMS;
- 5             c.     analyzing said ions to determine the molecular weight and abundance of said ions;
- 6             d.     determining the molecular structure of each species by multiple stages of mass  
7                     spectrometry; and
- 8             e.     producing a profile of the sample showing structure and concentration data for each  
9                     species.

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11     **5. (Original)**     A method according to claim 4, wherein said determining of the molecular weight is  
12     performed with an accuracy sufficient to identify empirical formula of said ions.

1        6. **(Currently Amended)**     A method for analyzing a ~~complex~~ biological sample using a Fourier  
2        Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 3            a.        ionizing a drug-dosed biological ~~the~~ sample to produce sample precursor ions;
- 4            b.        introducing said ions into the analysis region of said FTMS;
- 5            c.        analyzing said ions to determine the molecular weight, the abundance and the empirical  
6                      formula of said ions;
- 7            d.        fragmenting said sample precursor ions to produce fragment ions;
- 8            e.        determining the molecular weight, the abundance and empirical formula of said fragment  
9                      ions;
- 10           f.        determining the structure of said fragment ions by comparing said empirical formulas of  
11                      said fragment ions to a database of fragments with known structure;
- 12           g.        combining said structures of said fragment ions to determine the precursor ion structure  
13                      for each species in said sample; and
- 14           h.        producing a profile of said sample showing structure and concentration data for  
15                      selected species of said sample.

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17        7. **(Original)** A method according to claim 6, wherein said determining of the molecular weight is  
18        performed with an accuracy sufficient to identify empirical formula of said ions.

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20        8. **(Original)** A method according to claim 6, wherein said fragmenting is performed using  
21        photodissociation.

1 9. **(Currently Amended)** A method for analyzing a ~~complex~~ biological sample utilizing Fourier  
2 Transform Mass Spectrometry (FTMS), said method comprising the steps of:

- 3 a. ionizing polar molecules from a drug-dosed biological sample using positive and  
4 negative electrospray to produce sample (molecular) ions;  
5 b. introducing said ions into an analysis region of said FTMS;  
6 c. analyzing said ions to determine the molecular weight and abundance of said ions;  
7 d. utilizing said molecular weight to determine the empirical formula of each species of said  
8 sample; and  
9 e. identifying each said species by comparing said empirical formula to a database of  
10 formulas for known molecules.

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12 10. **(Original)** A method according to claim 9, wherein said determining of the molecular weight is  
13 performed with an accuracy sufficient to identify empirical formula of said ions.

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15 11. **(Currently Amended)** A method according to claim 9, wherein said database of known  
16 molecules is updated with said determined ~~molecular structures~~ empirical formulas.

12. (**Currently Amended**) A method for analyzing a ~~complex~~ biological sample utilizing Fourier Transform Mass Spectrometry (FTMS), said method comprising the steps of:

- a. ionizing non-polar molecules from a drug-dosed biological sample using positive and negative ion atmospheric pressure chemical ionization to produce sample (molecular) ions[.];
- b. introducing said ions into an analysis region of said FTMS;
- c. analyzing said ions to determine the molecular weight and abundance of said ions;
- d. utilizing said molecular weight to determine the empirical formula of each species of said sample; and
- e. identifying each said species by comparing said empirical formula to a database of formulas for known molecules.

13. (**Original**) A method according to claim 12, wherein said determining of the molecular weight is performed with an accuracy sufficient to identify empirical formula of said ions.

14. (**Currently Amended**) A method according to claim 12, wherein said database of known molecules is updated with said determined ~~molecular structures~~ empirical formulas.

15. (**New**) A method according to claim 1, wherein said a drug is injected into said biological sample to create said drug-dosed biological sample.

1 16. (New) A method according to claim 1, wherein metabolic products are detected.

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3 17. (New) A method according to claim 1, wherein cellular changes of said drug-dosed biological  
4 sample are identified.

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6 18. (New) A method according to claim 4, wherein said a drug is injected into said biological sample to  
7 create said drug-dosed biological sample.

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9 19. (New) A method according to claim 4, wherein metabolic products are detected.

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11 20. (New) A method according to claim 4, wherein cellular changes of said drug-dosed biological  
12 sample are identified.

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14 21. (New) A method according to claim 6, wherein said a drug is injected into said biological sample to  
15 create said drug-dosed biological sample.

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17 22. (New) A method according to claim 6, wherein metabolic products are detected.

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19 23. (New) A method according to claim 6, wherein cellular changes of said drug-dosed biological  
20 sample are identified.

1 24. (New) A method according to claim 9, wherein said a drug is injected into said biological sample to  
2 create said drug-dosed biological sample.

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4 25. (New) A method according to claim 9, wherein metabolic products are detected.

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6 26. (New) A method according to claim 9, wherein cellular changes of said drug-dosed biological  
7 sample are identified.

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9 27. (New) A method according to claim 12, wherein said a drug is injected into said biological sample  
10 to create said drug-dosed biological sample.

11  
12 28. (New) A method according to claim 12, wherein metabolic products are detected.

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14 29. (New) A method according to claim 12, wherein cellular changes of said drug-dosed biological  
15 sample are identified.--